

Alexander Zelikovsky

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

245
papers

3,194
citations

29
h-index

50
g-index

326
ext. papers

4,128
ext. citations

3.2
avg, IF

5.25
L-index

#	Paper	IF	Citations
245	A Novel Network Representation of SARS-CoV-2 Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2021 , 165-175	0.9	0
244	From Alpha to Zeta: Identifying Variants and Subtypes of SARS-CoV-2 Via Clustering. <i>Journal of Computational Biology</i> , 2021 , 28, 1113-1129	1.7	6
243	Scalable Reconstruction of SARS-CoV-2 Phylogeny with Recurrent Mutations. <i>Journal of Computational Biology</i> , 2021 , 28, 1130-1141	1.7	0
242	Quantitative differences between intra-host HCV populations from persons with recently established and persistent infections. <i>Virus Evolution</i> , 2021 , 7, veaa103	3.7	4
241	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. <i>Nucleic Acids Research</i> , 2021 , 49, e102	20.1	15
240	Epidemiological data analysis of viral quasispecies in the next-generation sequencing era. <i>Briefings in Bioinformatics</i> , 2021 , 22, 96-108	13.4	22
239	Clustering Based Identification of SARS-CoV-2 Subtypes. <i>Lecture Notes in Computer Science</i> , 2021 , 127-141	1.9	3
238	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021 , 22, 249	18.3	7
237	Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data. <i>Journal of Computational Biology</i> , 2021 , 28, 842-855	1.7	1
236	Computational Approaches to Detect Illicit Drug Ads and Find Vendor Communities Within Social Media Platforms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 ,	3	2
235	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020 , 21, 71	18.3	11
234	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. <i>Nature Communications</i> , 2020 , 11, 3126	17.4	12
233	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020 , 21, 31	18.3	274
232	Analysis of heterogeneous genomic samples using image normalization and machine learning. <i>BMC Genomics</i> , 2020 , 21, 405	4.5	2
231	Inference of mutability landscapes of tumors from single cell sequencing data. <i>PLoS Computational Biology</i> , 2020 , 16, e1008454	5	2
230	Global transmission network of SARS-CoV-2: from outbreak to pandemic 2020 ,		11
229	Using earth mover's distance for viral outbreak investigations. <i>BMC Genomics</i> , 2020 , 21, 582	4.5	5

228	Preface Special Issue: 15th International Symposium on Bioinformatics Research and Applications (ISBRA 2019). <i>Journal of Computational Biology</i> , 2020 , 27, 131-132	1.7	
227	Preface: 14th International Symposium on Bioinformatics Research and Applications (ISBRA 2018). <i>Journal of Computational Biology</i> , 2019 , 26, 767-768	1.7	
226	Guest Editors Introduction to the Special Section on Bioinformatics Research and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1362-1363	3	
225	Delineating Surface Epitopes of Lyme Disease Pathogen Targeted by Highly Protective Antibodies of New Zealand White Rabbits. <i>Infection and Immunity</i> , 2019 , 87,	3.7	2
224	New Zealand White Rabbits Effectively Clear <i>Borrelia burgdorferi</i> B31 despite the Bacterium's Functional Antigenic Variation System. <i>Infection and Immunity</i> , 2019 , 87,	3.7	3
223	Systematic benchmarking of omics computational tools. <i>Nature Communications</i> , 2019 , 10, 1393	17.4	62
222	Inference of clonal selection in cancer populations using single-cell sequencing data. <i>Bioinformatics</i> , 2019 , 35, i398-i407	7.2	5
221	Detecting Illicit Drug Ads in Google+ Using Machine Learning. <i>Lecture Notes in Computer Science</i> , 2019 , 171-179	0.9	1
220	Special Issue Preface: 13th International Symposium on Bioinformatics Research and Applications (ISBRA 2017). <i>Journal of Computational Biology</i> , 2018 , 25, 251-252	1.7	
219	Repeat-aware evaluation of scaffolding tools. <i>Bioinformatics</i> , 2018 , 34, 2530-2537	7.2	4
218	QUENTIN: reconstruction of disease transmissions from viral quasispecies genomic data. <i>Bioinformatics</i> , 2018 , 34, 163-170	7.2	35
217	Predicting Opioid Epidemic by Using Twitter Data. <i>Lecture Notes in Computer Science</i> , 2018 , 314-318	0.9	2
216	Identification of Surface Epitopes Associated with Protection against Highly Immune-Evasive VlsE-Expressing Lyme Disease Spirochetes. <i>Infection and Immunity</i> , 2018 , 86,	3.7	5
215	Fast estimation of genetic relatedness between members of heterogeneous populations of closely related genomic variants. <i>BMC Bioinformatics</i> , 2018 , 19, 360	3.6	3
214	Automated quality control for a molecular surveillance system. <i>BMC Bioinformatics</i> , 2018 , 19, 358	3.6	2
213	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Journal of Computational Biology</i> , 2017 , 24, 558-570	1.7	10
212	GaussianCpG: a Gaussian model for detection of CpG island in human genome sequences. <i>BMC Genomics</i> , 2017 , 18, 392	4.5	7
211	Metabolic Analysis of Metatranscriptomic Data from Planktonic Communities. <i>Lecture Notes in Computer Science</i> , 2017 , 396-402	0.9	1

210	Fast bootstrapping-based estimation of confidence intervals of expression levels and differential expression from RNA-Seq data. <i>Bioinformatics</i> , 2017 , 33, 3302-3304	7.2	27
209	HapIso: An Accurate Method for the Haplotype- Specific Isoforms Reconstruction From Long Single-Molecule Reads. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 108-115	3.4	6
208	Guest Editorial Introduction to the Special Issue on Bioinformatics Research and Applications. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 79-80	3.4	
207	Inference of genetic relatedness between viral quasispecies from sequencing data. <i>BMC Genomics</i> , 2017 , 18, 918	4.5	18
206	Identification of cancer-specific motifs in mimotope profiles of serum antibody repertoire. <i>BMC Bioinformatics</i> , 2017 , 18, 244	3.6	5
205	Antibody Response to Lyme Disease Spirochetes in the Context of VlsE-Mediated Immune Evasion. <i>Infection and Immunity</i> , 2017 , 85,	3.7	8
204	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 576-577	3	
203	Assessment of HCV infection stage as recent or chronic using multi-parameter analysis and machine learning 2017 ,		2
202	Modeling the Spread of HIV and HCV Infections Based on Identification and Characterization of High-Risk Communities Using Social Media. <i>Lecture Notes in Computer Science</i> , 2017 , 425-430	0.9	1
201	Agent-Based in Silico Evolution of HCV Quasispecies. <i>Lecture Notes in Computer Science</i> , 2017 , 420-424	0.9	
200	2016 ,		6
199	Genomic Variants Detection and Genotyping 2016 , 133-147		
198	Computing and Combinatorics. <i>Algorithmica</i> , 2016 , 76, 865-866	0.9	
197	Computational Methods for Transcript Assembly from RNA-SEQ Reads 2016 , 245-268		0
196	HapIso: An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads. <i>Lecture Notes in Computer Science</i> , 2016 , 80-92	0.9	
195	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Lecture Notes in Computer Science</i> , 2016 , 164-175	0.9	1
194	Wiley Series on Bioinformatics: Computational Techniques and Engineering 2016 , 1-2		
193	Influence of symbiont-produced bioactive natural products on holobiont fitness in the marine bryozoan, <i>Bugula neritina</i> via protein kinase C (PKC). <i>Marine Biology</i> , 2016 , 163, 1	2.5	5

- 192 Introduction to the Analysis of Environmental Sequence Information Using Metapathways **2016**, 25-56 1
- 191 Inferring metabolic pathway activity levels from RNA-Seq data. *BMC Genomics*, **2016**, 17 Suppl 5, 542 4.5 8
- 190 Cloud Computing for Next-Generation Sequencing Data Analysis **2016**, 1-24
- 189 Computational Approaches for Studying Alternative Splicing in Nonmodel Organisms from RNA-SEQ Data **2016**, 287-299
- 188 Pooling Strategy for Massive Viral Sequencing **2016**, 57-83
- 187 Applications of High-Fidelity Sequencing Protocol to RNA Viruses **2016**, 85-104
- 186 Scaffolding Algorithms **2016**, 105-131 3
- 185 Discovering and Genotyping Twilight Zone Deletions **2016**, 149-173
- 184 Computational Approaches for Finding Long Insertions and Deletions with NGS Data **2016**, 175-195
- 183 Computational Approaches in Next-Generation Sequencing Data Analysis for Genome-Wide DNA Methylation Studies **2016**, 197-226
- 182 Bisulfite-Conversion-Based Methods for DNA Methylation Sequencing Data Analysis **2016**, 227-243 1
- 181 An Overview And Comparison of Tools for RNA-Seq Assembly **2016**, 269-286
- 180 Transcriptome Quantification and Differential Expression from NGS Data **2016**, 301-327 1
- 179 Error Correction of NGS Reads from Viral Populations **2016**, 329-353 2
- 178 Probabilistic Viral Quasispecies Assembly **2016**, 355-381
- 177 Reconstruction of Infectious Bronchitis Virus Quasispecies from NGS Data **2016**, 383-400 1
- 176 Microbiome Analysis: State of the Art and Future Trends **2016**, 401-424 3
- 175 ScaffMatch: scaffolding algorithm based on maximum weight matching. *Bioinformatics*, **2015**, 31, 2632-87.2 31

174	ScaffMatch: Scaffolding Algorithm Based on Maximum Weight Matching. <i>Lecture Notes in Computer Science</i> , 2015 , 222-223	0.9	1
173	Computational framework for next-generation sequencing of heterogeneous viral populations using combinatorial pooling. <i>Bioinformatics</i> , 2015 , 31, 682-90	7.2	14
172	Searching High-Order SNP Combinations for Complex Diseases Based on Energy Distribution Difference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 695-704	3	11
171	GaussianCpG: A Gaussian model for detection of human CpG island 2015 ,		1
170	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. <i>BMC Genomics</i> , 2014 , 15 Suppl 5, S7	4.5	10
169	Bootstrap-based differential gene expression analysis for RNA-Seq data with and without replicates. <i>BMC Genomics</i> , 2014 , 15 Suppl 8, S2	4.5	35
168	Deterministic regression algorithm for transcriptome frequency estimation 2014 ,		1
167	VGA: A method for viral quasispecies assembly from ultra-deep sequencing data 2014 ,		1
166	Accurate viral population assembly from ultra-deep sequencing data. <i>Bioinformatics</i> , 2014 , 30, i329-37	7.2	42
165	Detection of genetic relatedness between viral samples using EM-based clustering of next-generation sequencing data 2014 ,		2
164	ILP-based maximum likelihood genome scaffolding. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 9, S9	3.6	5
163	Reconstruction of viral population structure from next-generation sequencing data using multicommodity flows. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 9, S2	3.6	19
162	Distributed Algorithms for TDMA Link Scheduling in Sensor Networks. <i>International Journal of Networking and Computing</i> , 2013 , 3, 55-74	0.2	4
161	Efficient Alignments of Metabolic Networks with Bounded Treewidth 2013 , 413-429		
160	kGEM: An EM-based algorithm for local reconstruction of viral quasispecies 2013 ,		2
159	Monte-Carlo Regression algorithm for isoform frequency estimation from RNA-Seq data 2013 ,		1
158	Alignment of DNA Mass-Spectral Profiles Using Network Flows. <i>Lecture Notes in Computer Science</i> , 2013 , 149-160	0.9	
157	Efficient error correction for next-generation sequencing of viral amplicons. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 10, S6	3.6	73

156	Maximum Series-Parallel Subgraph. <i>Algorithmica</i> , 2012 , 63, 137-157	0.9	3
155	Distributed Algorithms for TDMA Link Scheduling in Sensor Networks 2012 ,		1
154	Scalable genome scaffolding using integer linear programming 2012 ,		4
153	An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads 2012 ,		12
152	Optimal Testing of Digital Microfluidic Biochips. <i>INFORMS Journal on Computing</i> , 2011 , 23, 518-529	2.4	11
151	Estimation of alternative splicing isoform frequencies from RNA-Seq data. <i>Algorithms for Molecular Biology</i> , 2011 , 6, 9	1.8	125
150	Inferring viral quasispecies spectra from 454 pyrosequencing reads. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 6, S1	3.6	79
149	Collaborative Topology Control for Lifetime Maximization 2011 ,		4
148	Viral quasispecies reconstruction from amplicon 454 pyrosequencing reads 2011 ,		9
147	Reconstructing viral quasispecies from NGS amplicon reads. <i>In Silico Biology</i> , 2011 , 11, 237-49	2	12
146	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. <i>In Silico Biology</i> , 2011 , 11, 251-61	2	4
145	Maximum Likelihood Estimation of Incomplete Genomic Spectrum from HTS Data. <i>Lecture Notes in Computer Science</i> , 2011 , 213-224	0.9	0
144	Combinatorial Optimization Algorithms for Metabolic Networks Alignments and Their Applications. <i>International Journal of Knowledge Discovery in Bioinformatics</i> , 2011 , 2, 1-23		
143	Handbook of Approximation Algorithms and Metaheuristics. <i>Computer Journal</i> , 2010 , 53, 1338-1339	1.3	
142	Efficient Alignments of Metabolic Networks with Bounded Treewidth 2010 ,		2
141	Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data. <i>Lecture Notes in Computer Science</i> , 2010 , 202-214	0.9	11
140	A 3/2-Approximation Algorithm for Generalized Steiner Trees in Complete Graphs with Edge Lengths 1 and 2. <i>Lecture Notes in Computer Science</i> , 2010 , 15-24	0.9	
139	MetNetAligner: a web service tool for metabolic network alignments. <i>Bioinformatics</i> , 2009 , 25, 1989-90	7.2	15

138	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009 , 6, 178-179	3	
137	Mean Square Residue Biclustering with Missing Data and Row Inversions. <i>Lecture Notes in Computer Science</i> , 2009 , 28-39	0.9	4
136	1.25-Approximation Algorithm for Steiner Tree Problem with Distances 1 and 2. <i>Lecture Notes in Computer Science</i> , 2009 , 86-97	0.9	1
135	Genotype Tagging with Limited Overfitting. <i>Lecture Notes in Computer Science</i> , 2009 , 1-12	0.9	1
134	Fast Alignments of Metabolic Networks 2008 ,		6
133	2SNP: scalable phasing method for trios and unrelated individuals. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008 , 5, 313-8	3	7
132	Design and validation of methods searching for risk factors in genotype case-control studies. <i>Journal of Computational Biology</i> , 2008 , 15, 81-90	1.7	7
131	HCV Quasispecies Assembly Using Network Flows 2008 , 159-170		19
130	Guest editors' introduction to the special section on bioinformatics research and applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008 , 5, 321-2	3	
129	Discrete Methods for Association Search and Status Prediction in Genotype Case-Control Studies 2007 ,		1
128	Association testing by haplotype-sharing methods applicable to whole-genome analysis. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S129	2.3	11
127	2007 ,		4
126	Meta-Analysis of Microarray Data 2007 , 329-352		
125	Phasing Genotypes Using a Hidden Markov Model 2007 , 353-372		
124	Analytical and Algorithmic Methods for Haplotype Frequency Inference: What do they Tell Us? 2007 , 373-394		
123	Optimization Methods for Genotype Data Analysis in Epidemiological Studies 2007 , 395-415		
122	Topological Indices in Combinatorial Chemistry 2007 , 417-438		1
121	Efficient Algorithms for Structural Recall in Databases 2007 , 439-463		

120	Computational Approaches to Predict Protein-Protein and Domain-Domain Interactions 2007 , 465-491	1
119	Educating Biologists in the 21st Century: Bioinformatics Scientists versus Bioinformatics Technicians 2007 , 1-5	
118	Efficient Combinatorial Algorithms for DNA Sequence Processing 2007 , 223-239	
117	Algorithms for Multiplex PCR Primer Set Selection with Amplification Length Constraints 2007 , 241-258	0
116	Recent Developments in Alignment and Motif Finding for Sequences and Networks 2007 , 259-276	
115	Algorithms for Oligonucleotide Microarray Layout 2007 , 277-301	
114	Classification Accuracy Based Microarray Missing Value Imputation 2007 , 303-327	1
113	Dynamic Programming Algorithms for Biological Sequence and Structure Comparison 2007 , 7-28	1
112	Graph Theoretical Approaches to Delineate Dynamics of Biological Processes 2007 , 29-54	
111	Advances in Hidden Markov Models for Sequence Annotation 2007 , 55-91	2
110	Sorting- and FFT-Based Techniques in the Discovery of Biopatterns 2007 , 93-115	1
109	A Survey of Seeding for Sequence Alignment 2007 , 117-142	7
108	The Comparison of Phylogenetic Networks: Algorithms and Complexity 2007 , 143-173	2
107	Formal Models of Gene Clusters 2007 , 175-202	10
106	Integer Linear Programming Techniques for Discovering Approximate Gene Clusters 2007 , 203-221	1
105	Introduction to the Special Section on Computational Nanobioscience. <i>IEEE Transactions on Nanobioscience</i> , 2007 , 6, 1-3	3-4
104	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007 , 4, 513-514	3
103	Fast and Efficient Bright-Field AAPSM Conflict Detection and Correction. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2007 , 26, 115-126	2.5 8

102	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2007 , 26, 301-311	2.5	2
101	Informative SNP selection methods based on SNP prediction. <i>IEEE Transactions on Nanobioscience</i> , 2007 , 6, 60-7	3.4	17
100	A novel method for signal transduction network inference from indirect experimental evidence. <i>Journal of Computational Biology</i> , 2007 , 14, 927-49	1.7	43
99	A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence. <i>Lecture Notes in Computer Science</i> , 2007 , 407-419	0.9	1
98	Multiple linear regression for index SNP selection on unphased genotypes. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006 , 2006, 5759-62		2
97	2SNP: scalable phasing based on 2-SNP haplotypes. <i>Bioinformatics</i> , 2006 , 22, 371-3	7.2	36
96	MLR-tagging: informative SNP selection for unphased genotypes based on multiple linear regression. <i>Bioinformatics</i> , 2006 , 22, 2558-61	7.2	26
95	Combinatorial search methods for multi-SNP disease association. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2006 , 2006, 5802-5		12
94	Fill for Shallow Trench Isolation CMP. <i>IEEE/ACM International Conference on Computer-Aided Design, Digest of Technical Papers</i> , 2006 ,		2
93	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2006 , 25, 305-320	2.5	8
92	Fast yield driven fracture for variable shaped beam mask writing 2006 ,		8
91	Power Efficient Range Assignment for Symmetric Connectivity in Static Ad Hoc Wireless Networks. <i>Wireless Networks</i> , 2006 , 12, 287-299	2.5	61
90	Routing Using Messengers in Sparse and Disconnected Mobile Sensor Networks 2006 , 31-40		
89	Tag SNP Selection Based on Multivariate Linear Regression. <i>Lecture Notes in Computer Science</i> , 2006 , 750-757	0.9	4
88	Phasing of 2-SNP Genotypes Based on Non-random Mating Model. <i>Lecture Notes in Computer Science</i> , 2006 , 767-774	0.9	1
87	Applications of the Linear Matroid Parity Algorithm to Approximating Steiner Trees. <i>Lecture Notes in Computer Science</i> , 2006 , 70-79	0.9	2
86	Combinatorial Methods for Disease Association Search and Susceptibility Prediction. <i>Lecture Notes in Computer Science</i> , 2006 , 286-297	0.9	8
85	Compressible area fill synthesis. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2005 , 24, 1169-1187	2.5	4

84	Phasing and Missing Data Recovery in Family Trios. <i>Lecture Notes in Computer Science</i> , 2005 , 1011-1019	0.9	2
83	A combinatorial method for predicting genetic susceptibility to complex diseases. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2005 , 2006, 224-7		0
82	Tighter Bounds for Graph Steiner Tree Approximation. <i>SIAM Journal on Discrete Mathematics</i> , 2005 , 19, 122-134	0.7	187
81	Linear reduction method for predictive and informative tag SNP selection. <i>International Journal of Bioinformatics Research and Applications</i> , 2005 , 1, 249-60	0.9	7
80	Family trio phasing and missing data recovery. <i>International Journal of Bioinformatics Research and Applications</i> , 2005 , 1, 221-9	0.9	1
79	Improved Approximation Algorithms for the Quality of Service Multicast Tree Problem. <i>Algorithmica</i> , 2005 , 42, 109-120	0.9	8
78	The Polymatroid Steiner Problems. <i>Journal of Combinatorial Optimization</i> , 2005 , 9, 281-294	0.9	22
77	Transactions on Computational Systems Biology II. <i>Lecture Notes in Computer Science</i> , 2005 ,	0.9	7
76	Multi-project reticle floorplanning and wafer dicing 2004 ,		10
75	Scalable heuristics for design of DNA probe arrays. <i>Journal of Computational Biology</i> , 2004 , 11, 429-47	1.7	5
74	Consolidating software tools for DNA microarray design and manufacturing. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2004 , 2006, 172-5		1
73	Selecting Forwarding Neighbors in Wireless Ad Hoc Networks. <i>Mobile Networks and Applications</i> , 2004 , 9, 101-111	2.9	61
72	Linear reduction methods for tag SNP selection. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2004 , 2004, 2840-3		1
71	Yield- and cost-driven fracturing for variable shaped-beam mask writing 2004 ,		9
70	The Polymatroid Steiner Problems. <i>Lecture Notes in Computer Science</i> , 2004 , 234-245	0.9	
69	Linear Reduction for Haplotype Inference. <i>Lecture Notes in Computer Science</i> , 2004 , 242-253	0.9	4
68	SyD: A Middleware Testbed for Collaborative Applications over Small Heterogeneous Devices and Data Stores. <i>Lecture Notes in Computer Science</i> , 2004 , 352-371	0.9	5
67	Evaluation of placement techniques for DNA probe array layout 2003 ,		12

66	Improved Approximation Algorithms for the Quality of Service Steiner Tree Problem. <i>Lecture Notes in Computer Science</i> , 2003 , 401-411	0.9	2
65	The moving-target traveling salesman problem. <i>Journal of Algorithms</i> , 2003 , 49, 153-174		51
64	A New Approximation Algorithm for Finding Heavy Planar Subgraphs. <i>Algorithmica</i> , 2003 , 36, 179-205	0.9	8
63	Minimum buffered routing with bounded capacitive load for slew rate and reliability control. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2003 , 22, 241-253	2.5	12
62	On the skew-bounded minimum-buffer routing tree problem. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2003 , 22, 937-945	2.5	15
61	Engineering a scalable placement heuristic for DNA probe arrays 2003 ,		8
60	Network Lifetime and Power Assignment in ad hoc Wireless Networks. <i>Lecture Notes in Computer Science</i> , 2003 , 114-126	0.9	73
59	Monte-Carlo methods for chemical-mechanical planarization on multiple-layer and dual-material models 2002 ,		2
58	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2002 , 21, 263-274	2.5	6
57	Area fill synthesis for uniform layout density. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2002 , 21, 1132-1147	2.5	36
56	Auctions with Buyer Preferences. <i>IFIP Advances in Information and Communication Technology</i> , 2002 , 223-238	0.5	1
55	Border Length Minimization in DNA Array Design*. <i>Lecture Notes in Computer Science</i> , 2002 , 435-448	0.9	8
54	Symmetric Connectivity with Minimum Power Consumption in Radio Networks 2002 , 119-130		59
53	An improved approximation scheme for the Group Steiner Problem. <i>Networks</i> , 2001 , 37, 8-20	1.6	48
52	Hierarchical dummy fill for process uniformity 2001 ,		14
51	Provably good global buffering by multi-terminal multicommodity flow approximation 2001 ,		5
50	Practical Approximation Algorithms for Zero- and Bounded-Skew Trees. <i>SIAM Journal on Discrete Mathematics</i> , 2001 , 15, 97-111	0.7	3
49	Practical Approximation Algorithms for Separable Packing Linear Programs. <i>Lecture Notes in Computer Science</i> , 2001 , 325-337	0.9	1

48	A note on the MST heuristic for bounded edge-length Steiner trees with minimum number of Steiner points. <i>Information Processing Letters</i> , 2000 , 75, 165-167	0.8	21
47	Practical iterated fill synthesis for CMP uniformity 2000 ,		33
46	Optimal phase conflict removal for layout of dark field alternating phase shifting masks. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2000 , 19, 175-187	2.5	11
45	New approximation algorithms for routing with multiport terminals. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2000 , 19, 1118-1128	2.5	2
44	On Approximation of the Power-p and Bottleneck Steiner Trees. <i>Combinatorial Optimization</i> , 2000 , 117-135		2
43	Optimal phase conflict removal for layout of dark field alternating phase shifting masks 1999 ,		11
42	New multilevel and hierarchical algorithms for layout density control 1999 ,		6
41	New and exact filling algorithms for layout density control 1999 ,		12
40	Filling algorithms and analyses for layout density control. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 1999 , 18, 445-462	2.5	68
39	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 1999 , 18, 1265-1278	2.5	41
38	1999 ,		55
37	The T-join Problem in Sparse Graphs: Applications to Phase Assignment Problem in VLSI Mask Layout. <i>Lecture Notes in Computer Science</i> , 1999 , 25-36	0.9	2
36	Moving-Target TSP and Related Problems. <i>Lecture Notes in Computer Science</i> , 1998 , 453-464	0.9	12
35	Provably good routing tree construction with multi-port terminals 1997 ,		15
34	New Approximation Algorithms for the Steiner Tree Problems. <i>Journal of Combinatorial Optimization</i> , 1997 , 1, 47-65	0.9	95
33	A series of approximation algorithms for the acyclic directed steiner tree problem. <i>Algorithmica</i> , 1997 , 18, 99-110	0.9	72
32	Faster Approximation Algorithms for the Rectilinear Steiner Tree Problem. <i>Discrete and Computational Geometry</i> , 1997 , 18, 93-109	0.6	7
31	Spanning closed trail and hamiltonian cycle in grid graphs. <i>Lecture Notes in Computer Science</i> , 1995 , 342-351		2

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